

Substitute Sequence Listing

<110> DE VRIES, Erik
 GAFFAR, Fasilla Razzia
 YATSUDA, Ana Patricia
 SCHAAP, Theodorus Cornelis

<120> Pirop lasmid vaccine

<130> I-2003.010 US

<140>
 <141>

<150> PCT/EP2004/052169
 <151> 2004-09-14

<150> EP 03020898.7
 <151> 2003-09-14

<160> 20

<170> PatentIn version 3.3

<210> 1
 <211> 1818
 <212> DNA
 <213> Babesia bovis

<220>
 <221> CDS
 <222> (1)..(1818)

<400> 1	
atg cag tta cat aac aaa atg cag tca act tct ctc aaa tat aac tac	48
Met Gln Leu His Asn Lys Met Gln Ser Thr Ser Leu Lys Tyr Asn Tyr	
1 5 10 15	
aag cgc atg ctt tgt atg gct ctt gta cca gtt atc tta tcg tca ttt	96
Lys Arg Met Leu Cys Met Ala Leu Val Pro Val Ile Leu Ser Ser Phe	
20 25 30	
ttt gcg gaa gat gct tta gct tcc aac tcc acg ctt ttc gct ttc cac	144
Phe Ala Glu Asp Ala Leu Ala Ser Asn Ser Thr Leu Phe Ala Phe His	
35 40 45	
aag gaa cca aac aat cgt agg ctt acc aaa agg tct tca aga gga cag	192
Lys Glu Pro Asn Asn Arg Arg Leu Thr Lys Arg Ser Ser Arg Gly Gln	
50 55 60	
ttg ctc aac tca agg agg ggt tcg gat gat gcg tcc gaa tct tcc gat	240
Leu Leu Asn Ser Arg Arg Gly Ser Asp Asp Ala Ser Glu Ser Ser Asp	
65 70 75 80	
aga tac cca ggt agg tcg ggt ggc tct aag aat tcg agc caa tcc ccc	288
Arg Tyr Pro Gly Arg Ser Gly Gly Ser Lys Asn Ser Ser Gln Ser Pro	
85 90 95	
tgg atc aag tat atg caa aag ttc gac att ccc cgt aac cac ggc tct	336
Trp Ile Lys Tyr Met Gln Lys Phe Asp Ile Pro Arg Asn His Gly Ser	
100 105 110	

Substitute Sequence Listing

gga atc tat gtc gat ctt gga gga tat gaa tcc gtt ggt tca aaa agt Gly Ile Tyr Val Asp Leu Gly Gly Tyr Glu Ser Val Gly Ser Lys Ser	384
tat cgt atg ccc gtt ggt aag tgc cca gta gtc ggt aaa att ata gac Tyr Arg Met Pro Val Gly Lys Cys Pro Val Val Gly Lys Ile Ile Asp	432
ctt gga aat ggt gcc gac ttc ctc gat ccc att tca tca gac gac cca Leu Gly Asn Gly Ala Asp Phe Leu Asp Pro Ile Ser Ser Asp Asp Pro	480
agt tac cgt ggt ttg gca ttc ccc gag act gct gtg gac tct aat att Ser Tyr Arg Gly Leu Ala Phe Pro Glu Thr Ala Val Asp Ser Asn Ile	528
ccc aca caa cca aag aca cgt ggt tct tca tca gca tct gcg gcc aaa Pro Thr Gln Pro Lys Thr Arg Gly Ser Ser Ser Ala Ser Ala Ala Lys	576
tta tct cct gtt tcg gcg aaa gat ctg aga cgt tgg gga tat gaa ggt Leu Ser Pro Val Ser Ala Lys Asp Leu Arg Arg Trp Gly Tyr Glu Gly	624
aat gat gta gcg aat tgc tca gaa tat gct agt aac ctc att ccc gca Asn Asp Val Ala Asn Cys Ser Glu Tyr Ala Ser Asn Leu Ile Pro Ala	672
tca gac agg agt acc aaa tat agg tat cct ttt gtt ttt gac agt gat Ser Asp Arg Ser Thr Lys Tyr Arg Tyr Pro Phe Val Phe Asp Ser Asp	720
aac cag atg tgt tac ata ctg tac tct gcc ata caa tac aac caa gga Asn Gln Met Cys Tyr Ile Leu Tyr Ser Ala Ile Gln Tyr Asn Gln Gly	768
aat agg tat tgt gac aac gat ggt agc tcc gaa gat ggt aca agc tct Asn Arg Tyr Cys Asp Asn Asp Gly Ser Ser Glu Asp Gly Thr Ser Ser	816
ttg ctt tgc atg aaa cct tac aag agc gct gag gat gca cac tta tac Leu Leu Cys Met Lys Pro Tyr Lys Ser Ala Glu Asp Ala His Leu Tyr	864
tac ggt tct gcg aaa gtt gac ccc gat tgg gaa gaa aat tgt ccc atg Tyr Gly Ser Ala Lys Val Asp Pro Asp Trp Glu Glu Asn Cys Pro Met	912
cac ccg gta agg gat gcc att ttt ggt aaa tgg tct ggt ggc tct tgt His Pro Val Arg Asp Ala Ile Phe Gly Lys Trp Ser Gly Gly Ser Cys	960
ggt gcc att gct cct gca ttc caa gaa tat gcc aac agc act gaa gac Val Ala Ile Ala Pro Ala Phe Gln Glu Tyr Ala Asn Ser Thr Glu Asp	1008
tgt gca gcc att tta ttc gat aac tct gca act gac ttg aat atc gaa Cys Ala Ala Ile Leu Phe Asp Asn Ser Ala Thr Asp Leu Asn Ile Glu	1056
gct gtt aac gaa gat ttt aat gaa ctt aaa gaa ttg acc gat ggg ctt Ala Val Asn Glu Asp Phe Asn Glu Leu Lys Glu Leu Thr Asp Gly Leu	1104

355	Substitute Sequence Listing															
	360															
	365															
aaa aga ttg aac atg tcg aag gtt gca aac gct att ttt tct ccc ctc	1152															
Lys Arg Leu Asn Met Ser Lys Val Ala Asn Ala Ile Phe Ser Pro Leu																
370 375 380																
tcc aat gtt gca ggt acc agt cga att tca cgt ggt gtg ggt atg aac	1200															
Ser Asn Val Ala Gly Thr Ser Arg Ile Ser Arg Gly Val Gly Met Asn																
385 390 395 400																
tgg gct aca tac gat aaa gat tct ggt atg tgt gct ctc att aac gaa	1248															
Trp Ala Thr Tyr Asp Lys Asp Ser Gly Met Cys Ala Leu Ile Asn Glu																
405 410 415																
aca cct aac tgc ttg atc ttg aac gcg gga agc att gct ctc acg gct	1296															
Thr Pro Asn Cys Leu Ile Leu Asn Ala Gly Ser Ile Ala Leu Thr Ala																
420 425 430																
ata ggt tca cct ctc gag tat gac gct gtt aac tat cct tgc cac atc	1344															
Ile Gly Ser Pro Leu Glu Tyr Asp Ala Val Asn Tyr Pro Cys His Ile																
435 440 445																
gac acc aat ggt tac gtt gag cca cgt gca aag aat acc aac aaa tac	1392															
Asp Thr Asn Gly Tyr Val Glu Pro Arg Ala Lys Asn Thr Asn Lys Tyr																
450 455 460																
ctt gat gtt cct ttc gag gtc aca act gct ttg agc atg aag aca cta	1440															
Leu Asp Val Pro Phe Glu Val Thr Thr Ala Leu Ser Met Lys Thr Leu																
465 470 475 480																
aaa tgc gat gcc tat gtt cac acc aag tac tct gac agt tgt ggt acc	1488															
Lys Cys Asp Ala Tyr Val His Thr Lys Tyr Ser Asp Ser Cys Gly Thr																
485 490 495																
tat ttc ctt tgc tca gac gtc aaa cct aac tgg ttc att agg ttc tta	1536															
Tyr Phe Leu Cys Ser Asp Val Lys Pro Asn Trp Phe Ile Arg Phe Leu																
500 505 510																
cac atg atc gga ctc tac aac aca aag cgt atc gta ata ttc gtg tgc	1584															
His Met Ile Gly Leu Tyr Asn Thr Lys Arg Ile Val Ile Phe Val Cys																
515 520 525																
tgt acc act acc gcc atc gtt ctc act atc tgg ata tgg aaa cga ttc	1632															
Cys Thr Thr Ala Ile Val Leu Thr Ile Trp Ile Trp Lys Arg Phe																
530 535 540																
atc aag gct aag aaa gag ccg gcc cct cca agt ttc gac aaa tac cta	1680															
Ile Lys Ala Lys Lys Glu Pro Ala Pro Pro Ser Phe Asp Lys Tyr Leu																
545 550 555 560																
agc aac tat gat tat gat aca acc cta gat gcc gac aac gaa acg gaa	1728															
Ser Asn Tyr Asp Tyr Asp Thr Thr Leu Asp Ala Asp Asn Glu Thr Glu																
565 570 575																
cag cgt ttg gat tcc tct gct tat agc tgg gga gag gct gta caa aga	1776															
Gln Arg Leu Asp Ser Ser Ala Tyr Ser Trp Gly Glu Ala Val Gln Arg																
580 585 590																
cca agt gat gtc acc cct gta aaa ctc tct aaa atc aac taa	1818															
Pro Ser Asp Val Thr Pro Val Lys Leu Ser Lys Ile Asn																
595 600 605																

Substitute Sequence Listing

<210> 2
 <211> 605
 <212> PRT
 <213> Babesia bovis

<400> 2

Met Gln Leu His Asn Lys Met Gln Ser Thr Ser Leu Lys Tyr Asn Tyr
 1 5 10 15

Lys Arg Met Leu Cys Met Ala Leu Val Pro Val Ile Leu Ser Ser Phe
 20 25 30

Phe Ala Glu Asp Ala Leu Ala Ser Asn Ser Thr Leu Phe Ala Phe His
 35 40 45

Lys Glu Pro Asn Asn Arg Arg Leu Thr Lys Arg Ser Ser Arg Gly Gln
 50 55 60

Leu Leu Asn Ser Arg Arg Gly Ser Asp Asp Ala Ser Glu Ser Ser Asp
 65 70 75 80

Arg Tyr Pro Gly Arg Ser Gly Gly Ser Lys Asn Ser Ser Gln Ser Pro
 85 90 95

Trp Ile Lys Tyr Met Gln Lys Phe Asp Ile Pro Arg Asn His Gly Ser
 100 105 110

Gly Ile Tyr Val Asp Leu Gly Gly Tyr Glu Ser Val Gly Ser Lys Ser
 115 120 125

Tyr Arg Met Pro Val Gly Lys Cys Pro Val Val Gly Lys Ile Ile Asp
 130 135 140

Leu Gly Asn Gly Ala Asp Phe Leu Asp Pro Ile Ser Ser Asp Asp Pro
 145 150 155 160

Ser Tyr Arg Gly Leu Ala Phe Pro Glu Thr Ala Val Asp Ser Asn Ile
 165 170 175

Pro Thr Gln Pro Lys Thr Arg Gly Ser Ser Ser Ala Ser Ala Ala Lys
 180 185 190

Leu Ser Pro Val Ser Ala Lys Asp Leu Arg Arg Trp Gly Tyr Glu Gly
 195 200 205

Asn Asp Val Ala Asn Cys Ser Glu Tyr Ala Ser Asn Leu Ile Pro Ala
 210 215 220

Substitute Sequence Listing

Ser Asp Arg Ser Thr Lys Tyr Arg Tyr Pro Phe Val Phe Asp Ser Asp
225 230 235 240

Asn Gln Met Cys Tyr Ile Leu Tyr Ser Ala Ile Gln Tyr Asn Gln Gly
245 250 255

Asn Arg Tyr Cys Asp Asn Asp Gly Ser Ser Glu Asp Gly Thr Ser Ser
260 265 270

Leu Leu Cys Met Lys Pro Tyr Lys Ser Ala Glu Asp Ala His Leu Tyr
275 280 285

Tyr Gly Ser Ala Lys Val Asp Pro Asp Trp Glu Glu Asn Cys Pro Met
290 295 300

His Pro Val Arg Asp Ala Ile Phe Gly Lys Trp Ser Gly Gly Ser Cys
305 310 315 320

Val Ala Ile Ala Pro Ala Phe Gln Glu Tyr Ala Asn Ser Thr Glu Asp
325 330 335

Cys Ala Ala Ile Leu Phe Asp Asn Ser Ala Thr Asp Leu Asn Ile Glu
340 345 350

Ala Val Asn Glu Asp Phe Asn Glu Leu Lys Glu Leu Thr Asp Gly Leu
355 360 365

Lys Arg Leu Asn Met Ser Lys Val Ala Asn Ala Ile Phe Ser Pro Leu
370 375 380

Ser Asn Val Ala Gly Thr Ser Arg Ile Ser Arg Gly Val Gly Met Asn
385 390 395 400

Trp Ala Thr Tyr Asp Lys Asp Ser Gly Met Cys Ala Leu Ile Asn Glu
405 410 415

Thr Pro Asn Cys Leu Ile Leu Asn Ala Gly Ser Ile Ala Leu Thr Ala
420 425 430

Ile Gly Ser Pro Leu Glu Tyr Asp Ala Val Asn Tyr Pro Cys His Ile
435 440 445

Asp Thr Asn Gly Tyr Val Glu Pro Arg Ala Lys Asn Thr Asn Lys Tyr
450 455 460

Leu Asp Val Pro Phe Glu Val Thr Thr Ala Leu Ser Met Lys Thr Leu
465 470 475 480

Substitute Sequence Listing

Lys Cys Asp Ala Tyr Val His Thr Lys Tyr Ser Asp Ser Cys Gly Thr
485 490 495

Tyr Phe Leu Cys Ser Asp Val Lys Pro Asn Trp Phe Ile Arg Phe Leu
500 505 510

His Met Ile Gly Leu Tyr Asn Thr Lys Arg Ile Val Ile Phe Val Cys
515 520 525

Cys Thr Thr Thr Ala Ile Val Leu Thr Ile Trp Ile Trp Lys Arg Phe
530 535 540

Ile Lys Ala Lys Lys Glu Pro Ala Pro Pro Ser Phe Asp Lys Tyr Leu
545 550 555 560

Ser Asn Tyr Asp Tyr Asp Thr Thr Leu Asp Ala Asp Asn Glu Thr Glu
565 570 575

Gln Arg Leu Asp Ser Ser Ala Tyr Ser Trp Gly Glu Ala Val Gln Arg
580 585 590

Pro Ser Asp Val Thr Pro Val Lys Leu Ser Lys Ile Asn
595 600 605

<210> 3
<211> 2349
<212> DNA
<213> Theileria annulata

<220>
<221> CDS
<222> (1)..(2349)

<400> 3
atg aaa aaa ata gga ctt aaa att agg gca caa aag gat aaa tta aat 48
Met Lys Lys Ile Gly Leu Lys Ile Arg Ala Gln Lys Asp Lys Leu Asn
1 5 10 15

cct gtg tta gga agc aac tct gac cct tcg gaa gag tat gat tca ttc 96
Pro Val Leu Gly Ser Asn Ser Asp Pro Ser Glu Glu Tyr Asp Ser Phe
20 25 30

cag caa aat gtt ttc act cat caa cca acc caa cta cac aaa tct cat 144
Gln Gln Asn Val Phe Thr His Gln Pro Thr Gln Leu His Lys Ser His
35 40 45

cac tac att aca cac cag aaa aaa acc agc caa cac atc gac gat tta 192
His Tyr Ile Thr His Gln Lys Lys Thr Ser Gln His Ile Asp Asp Leu
50 55 60

aat ttt tat aat gga aaa ttt aat caa aag agc aga att ggt cca ggg 240
Asn Phe Tyr Asn Gly Lys Phe Asn Gln Lys Ser Arg Ile Gly Pro Gly
65 70 75 80

Substitute Sequence Listing

aag gta gta aat aac agt agg aat ctg gta gaa ggt gaa aca cta tct Lys Val Val Asn Asn Ser Arg Asn Leu Val Glu Gly Glu Thr Leu Ser 85 90 95	288
aag gat gac aat aaa aca aaa tct aaa ata aag tca aaa aca gca tca Lys Asp Asp Asn Lys Thr Lys Ser Lys Ile Lys Ser Lys Thr Ala Ser 100 105 110	336
att tta cct aga ctt tta aaa tct tta tca ttt tta gct gtt tta ggg Ile Leu Pro Arg Leu Leu Lys Ser Leu Ser Phe Leu Ala Val Leu Gly 115 120 125	384
tca att aat tca ttt tca tta gca tta gag gaa cct ttt act caa cac Ser Ile Asn Ser Phe Ser Leu Ala Leu Glu Glu Pro Phe Thr Gln His 130 135 140	432
act tct aac cga acg ccc ttt gaa gta tca tta att caa agc aac agc Thr Ser Asn Arg Thr Pro Phe Glu Val Ser Leu Ile Gln Ser Asn Ser 145 150 155 160	480
agt tta tcg cct att cat aat tct tca act caa aat tca agt cat cac Ser Leu Ser Pro Ile His Asn Ser Ser Thr Gln Asn Ser Ser His His 165 170 175	528
aac ggt ttt agt ggt agt acc gtt aat aat acc tca tta ata gag aca Asn Gly Phe Ser Gly Ser Thr Val Asn Asn Thr Ser Leu Ile Glu Thr 180 185 190	576
agg aat aac gta tta aac aga aca cta ggt aga ttc gga tca ttt ttg Arg Asn Asn Val Leu Asn Arg Thr Leu Gly Arg Phe Gly Ser Phe Leu 195 200 205	624
caa tca gga ttg ata agc agt aga gca gac aaa aag aag cgg tct ggt Gln Ser Gly Leu Ile Ser Ser Arg Ala Asp Lys Lys Lys Arg Ser Gly 210 215 220	672
atg aat aga aga ggc cct aag ggg aag aaa ggg aag gga gga gaa gac Met Asn Arg Arg Gly Pro Lys Gly Lys Lys Gly Lys Gly Glu Asp 225 230 235 240	720
gaa gaa aag agg aac aag tgg acc gat ttc atg gca aag ttt gat atc Glu Glu Lys Arg Asn Lys Trp Thr Asp Phe Met Ala Lys Phe Asp Ile 245 250 255	768
gct aag gtc cac ggt tca ggg gtt tac gta gat ttg ggt gaa tct gcc Ala Lys Val His Gly Ser Gly Val Tyr Val Asp Leu Gly Glu Ser Ala 260 265 270	816
acc gtt ggc agt tat gac tac agg atg cct ata gga aaa tgt cca gtt Thr Val Gly Ser Tyr Asp Tyr Arg Met Pro Ile Gly Lys Cys Pro Val 275 280 285	864
gta ggt aag gca atc ata ctc gag aat gga gct gat ttt ttg agc agc Val Gly Lys Ala Ile Ile Leu Glu Asn Gly Ala Asp Phe Leu Ser Ser 290 295 300	912
ata acc cat cat gac ccc aag gag aga ggg ctg ggg ttc cct gct aca Ile Thr His His Asp Pro Lys Glu Arg Gly Leu Gly Phe Pro Ala Thr 305 310 315 320	960
aaa gtt gcc tca aat tca tca aaa ctg gac atg gag aac cag ctc tta Lys Val Ala Ser Asn Ser Ser Lys Leu Asp Met Glu Asn Gln Leu Leu Page 7	1008

Substitute Sequence Listing

Substitute Sequence Listing																
325						330						335				
tca	cca	att	agt	gct	cag	gtc	cta	agg	agc	tgg	aat	tat	aaa	cac	gaa	1056
Ser	Pro	Ile	Ser	Ala	Gln	Val	Leu	Arg	Ser	Trp	Asn	Tyr	Lys	His	Glu	
			340				345			350						
tca	gat	tta	agt	aat	tgt	gct	gag	tat	tcg	aga	aac	att	gtt	ccg	ggc	1104
Ser	Asp	Leu	Ser	Asn	Cys	Ala	Glu	Tyr	Ser	Arg	Asn	Ile	Val	Pro	Gly	
			355				360			365						
agt	aat	cgt	aat	tca	aag	tat	cgt	tac	ccg	ttt	gta	tat	gat	gag	tct	1152
Ser	Asn	Arg	Asn	Ser	Lys	Tyr	Arg	Tyr	Pro	Phe	Val	Tyr	Asp	Glu	Ser	
			370				375			380						
gag	aag	ctt	tgt	tat	att	tta	tat	agt	ccc	atg	caa	tat	aat	cag	ggc	1200
Glu	Lys	Leu	Cys	Tyr	Ile	Leu	Tyr	Ser	Pro	Met	Gln	Tyr	Asn	Gln	Gly	
			385				390			395						400
gta	aag	tac	tgt	gac	caa	gac	tct	ccg	gac	gaa	gga	act	agc	agt	tta	1248
Val	Lys	Tyr	Cys	Asp	Gln	Asp	Ser	Pro	Asp	Glu	Gly	Thr	Ser	Ser	Leu	
			405				410						415			
gct	tgt	atg	tac	ccg	gat	aag	agc	aag	gag	gat	tca	cac	cta	ttt	tac	1296
Ala	Cys	Met	Tyr	Pro	Asp	Lys	Ser	Lys	Glu	Asp	Ser	His	Leu	Phe	Tyr	
			420				425						430			
gga	acc	agc	ggg	ctt	cac	atg	gac	tgg	cct	gta	ggt	tgc	cca	ggt	tac	1344
Gly	Thr	Ser	Gly	Leu	His	Met	Asp	Trp	Pro	Val	Val	Cys	Pro	Val	Tyr	
			435				440						445			
cct	att	aga	gat	tcg	att	ttt	gga	tcc	tac	gac	gac	caa	aag	gac	gaa	1392
Pro	Ile	Arg	Asp	Ser	Ile	Phe	Gly	Ser	Tyr	Asp	Asp	Gln	Lys	Asp	Glu	
			450				455			460						
tgt	ggt	cca	att	gag	ccg	ata	ttt	gag	gag	gag	gct	gaa	gat	tat	gag	1440
Cys	Val	Pro	Ile	Glu	Pro	Ile	Phe	Glu	Glu	Glu	Ala	Glu	Asp	Tyr	Glu	
			465				470			475						480
gca	tgt	gcc	aag	ata	att	ttc	gag	tat	tct	cca	agt	gat	ggt	gat	att	1488
Ala	Cys	Ala	Lys	Ile	Ile	Phe	Glu	Tyr	Ser	Pro	Ser	Asp	Val	Asp	Ile	
			485				490						495			
agc	aca	aat	aac	cag	aag	ctt	tca	gac	gtc	gac	ctt	tac	aag	gag	gcg	1536
Ser	Thr	Asn	Asn	Gln	Lys	Leu	Ser	Asp	Val	Asp	Leu	Tyr	Lys	Glu	Ala	
			500				505			510						
atg	aat	aat	gga	aag	ctg	agc	act	gct	ctt	tca	att	atg	ttt	gct	cct	1584
Met	Asn	Asn	Gly	Lys	Leu	Ser	Thr	Ala	Leu	Ser	Ile	Met	Phe	Ala	Pro	
			515				520			525						
agg	tac	tct	gag	gat	cgt	ccg	atc	tat	act	aaa	ggg	gtc	ggg	ata	aac	1632
Arg	Tyr	Ser	Glu	Asp	Arg	Pro	Ile	Tyr	Thr	Lys	Gly	Val	Gly	Ile	Asn	
			530				535			540						
tgg	gct	aca	tac	tcc	gtc	gag	gaa	aag	aaa	tgt	aac	att	ctc	gac	ggt	1680
Trp	Ala	Thr	Tyr	Ser	Val	Glu	Glu	Lys	Lys	Cys	Asn	Ile	Leu	Asp	Val	
			545				550			555						560
ggt	ccc	agc	tgt	ctt	att	ata	agt	aac	ggc	cac	tat	gcc	ctt	aca	agt	1728
Val	Pro	Ser	Cys	Leu	Ile	Ile	Ser	Asn	Gly	His	Tyr	Ala	Leu	Thr	Ser	
			565				570			575						
ctc	agc	tca	ccc	aat	gaa	gag	gat	gct	ata	aat	tac	ccc	tgc	gat	atc	1776

Substitute Sequence Listing															
Leu	Ser	Ser	Pro	Asn	Glu	Glu	Asp	Ala	Ile	Asn	Tyr	Pro	Cys	Asp	Ile
			580					585					590		
gtt	cag	ggc	aag	ggg	ttt	ttg	aag	aac	cca	aac	ggt	gga	aaa	aag	aat
Val	Gln	Gly	Lys	Gly	Phe	Leu	Lys	Asn	Pro	Asn	Gly	Gly	Lys	Lys	Asn
		595					600					605			
gct	cag	gaa	ccg	ccc	aag	gaa	cct	gaa	cct	gaa	gaa	cct	aag	aag	gag
Ala	Gln	Glu	Pro	Pro	Lys	Glu	Pro	Glu	Pro	Glu	Glu	Pro	Lys	Lys	Glu
	610					615					620				
ggt	gct	gaa	aac	aaa	ccc	aaa	gag	aaa	ggt	aaa	tct	gag	aaa	aag	aat
Gly	Ala	Glu	Asn	Lys	Pro	Lys	Glu	Lys	Gly	Lys	Ser	Glu	Lys	Lys	Asn
625					630					635					640
gaa	aaa	tct	atg	cct	tca	gga	cca	ttc	acg	cca	tac	act	agc	ttg	aag
Glu	Lys	Ser	Met	Pro	Ser	Gly	Pro	Phe	Thr	Pro	Tyr	Thr	Ser	Leu	Lys
				645					650					655	
aag	gag	ggt	ttc	gag	tgc	agt	aaa	tac	act	ggt	gag	cgg	gtg	aac	aaa
Lys	Glu	Gly	Phe	Glu	Cys	Ser	Lys	Tyr	Thr	Val	Glu	Arg	Val	Asn	Lys
			660					665					670		
agc	tgc	ggc	gtt	tac	tat	gaa	tgc	tca	gaa	acg	cct	gta	tta	ttt	acc
Ser	Cys	Gly	Val	Tyr	Tyr	Glu	Cys	Ser	Glu	Thr	Pro	Val	Leu	Phe	Thr
		675					680					685			
aag	aag	aat	agg	att	tat	cta	tac	atc	ata	ttg	gca	gta	tcg	ctt	gta
Lys	Lys	Asn	Arg	Ile	Tyr	Leu	Tyr	Ile	Ile	Leu	Ala	Val	Ser	Leu	Val
	690					695					700				
gta	ctg	gcc	gtc	tta	gcc	tac	ttt	gga	tac	agg	tac	tac	agt	aag	aat
Val	Leu	Ala	Val	Leu	Ala	Tyr	Phe	Gly	Tyr	Arg	Tyr	Tyr	Ser	Lys	Asn
705					710					715					720
cac	ttg	aaa	aaa	cac	aat	tcc	cag	ata	tat	gaa	gat	gat	aac	gtg	aac
His	Leu	Lys	Lys	His	Asn	Ser	Gln	Ile	Tyr	Glu	Asp	Asp	Asn	Val	Asn
				725					730					735	
aac	tac	tac	aat	gag	gac	ttt	gat	gac	gaa	caa	gat	cgg	gat	gaa	tac
Asn	Tyr	Tyr	Asn	Glu	Asp	Phe	Asp	Asp	Glu	Gln	Asp	Arg	Asp	Glu	Tyr
			740					745					750		
gct	tcg	aat	gtt	aga	ggt	gat	caa	atc	tgg	agc	aga	cac	act	cca	gac
Ala	Ser	Asn	Val	Arg	Gly	Asp	Gln	Ile	Trp	Ser	Arg	His	Thr	Pro	Asp
		755					760					765			
aga	tct	gaa	gtt	act	cca	gtc	aga	atc	tct	agg	tta	aac	cat	taa	
Arg	Ser	Glu	Val	Thr	Pro	Val	Arg	Ile	Ser	Arg	Leu	Asn	His		
	770					775					780				

<210> 4
 <211> 782
 <212> PRT
 <213> Theileria annulata

<400> 4

Met Lys Lys Ile Gly Leu Lys Ile Arg Ala Gln Lys Asp Lys Leu Asn
 1 5 10 15

Substitute Sequence Listing

Pro Val Leu Gly Ser Asn Ser Asp Pro Ser Glu Glu Tyr Asp Ser Phe
20 25 30

Gln Gln Asn Val Phe Thr His Gln Pro Thr Gln Leu His Lys Ser His
35 40 45

His Tyr Ile Thr His Gln Lys Lys Thr Ser Gln His Ile Asp Asp Leu
50 55 60

Asn Phe Tyr Asn Gly Lys Phe Asn Gln Lys Ser Arg Ile Gly Pro Gly
65 70 75 80

Lys Val Val Asn Asn Ser Arg Asn Leu Val Glu Gly Glu Thr Leu Ser
85 90 95

Lys Asp Asp Asn Lys Thr Lys Ser Lys Ile Lys Ser Lys Thr Ala Ser
100 105 110

Ile Leu Pro Arg Leu Leu Lys Ser Leu Ser Phe Leu Ala Val Leu Gly
115 120 125

Ser Ile Asn Ser Phe Ser Leu Ala Leu Glu Glu Pro Phe Thr Gln His
130 135 140

Thr Ser Asn Arg Thr Pro Phe Glu Val Ser Leu Ile Gln Ser Asn Ser
145 150 155 160

Ser Leu Ser Pro Ile His Asn Ser Ser Thr Gln Asn Ser Ser His His
165 170 175

Asn Gly Phe Ser Gly Ser Thr Val Asn Asn Thr Ser Leu Ile Glu Thr
180 185 190

Arg Asn Asn Val Leu Asn Arg Thr Leu Gly Arg Phe Gly Ser Phe Leu
195 200 205

Gln Ser Gly Leu Ile Ser Ser Arg Ala Asp Lys Lys Lys Arg Ser Gly
210 215 220

Met Asn Arg Arg Gly Pro Lys Gly Lys Lys Gly Lys Gly Gly Glu Asp
225 230 235 240

Glu Glu Lys Arg Asn Lys Trp Thr Asp Phe Met Ala Lys Phe Asp Ile
245 250 255

Ala Lys Val His Gly Ser Gly Val Tyr Val Asp Leu Gly Glu Ser Ala
260 265 270

Substitute Sequence Listing

Thr Val Gly Ser Tyr Asp Tyr Arg Met Pro Ile Gly Lys Cys Pro Val
275 280 285

Val Gly Lys Ala Ile Ile Leu Glu Asn Gly Ala Asp Phe Leu Ser Ser
290 295 300

Ile Thr His His Asp Pro Lys Glu Arg Gly Leu Gly Phe Pro Ala Thr
305 310 315 320

Lys Val Ala Ser Asn Ser Ser Lys Leu Asp Met Glu Asn Gln Leu Leu
325 330 335

Ser Pro Ile Ser Ala Gln Val Leu Arg Ser Trp Asn Tyr Lys His Glu
340 345 350

Ser Asp Leu Ser Asn Cys Ala Glu Tyr Ser Arg Asn Ile Val Pro Gly
355 360 365

Ser Asn Arg Asn Ser Lys Tyr Arg Tyr Pro Phe Val Tyr Asp Glu Ser
370 375 380

Glu Lys Leu Cys Tyr Ile Leu Tyr Ser Pro Met Gln Tyr Asn Gln Gly
385 390 395 400

Val Lys Tyr Cys Asp Gln Asp Ser Pro Asp Glu Gly Thr Ser Ser Leu
405 410 415

Ala Cys Met Tyr Pro Asp Lys Ser Lys Glu Asp Ser His Leu Phe Tyr
420 425 430

Gly Thr Ser Gly Leu His Met Asp Trp Pro Val Val Cys Pro Val Tyr
435 440 445

Pro Ile Arg Asp Ser Ile Phe Gly Ser Tyr Asp Asp Gln Lys Asp Glu
450 455 460

Cys Val Pro Ile Glu Pro Ile Phe Glu Glu Glu Ala Glu Asp Tyr Glu
465 470 475 480

Ala Cys Ala Lys Ile Ile Phe Glu Tyr Ser Pro Ser Asp Val Asp Ile
485 490 495

Ser Thr Asn Asn Gln Lys Leu Ser Asp Val Asp Leu Tyr Lys Glu Ala
500 505 510

Met Asn Asn Gly Lys Leu Ser Thr Ala Leu Ser Ile Met Phe Ala Pro
515 520 525

Substitute Sequence Listing

Arg Tyr Ser Glu Asp Arg Pro Ile Tyr Thr Lys Gly Val Gly Ile Asn
530 535 540

Trp Ala Thr Tyr Ser Val Glu Glu Lys Lys Cys Asn Ile Leu Asp Val
545 550 555 560

Val Pro Ser Cys Leu Ile Ile Ser Asn Gly His Tyr Ala Leu Thr Ser
565 570 575

Leu Ser Ser Pro Asn Glu Glu Asp Ala Ile Asn Tyr Pro Cys Asp Ile
580 585 590

Val Gln Gly Lys Gly Phe Leu Lys Asn Pro Asn Gly Gly Lys Lys Asn
595 600 605

Ala Gln Glu Pro Pro Lys Glu Pro Glu Pro Glu Glu Pro Lys Lys Glu
610 615 620

Gly Ala Glu Asn Lys Pro Lys Glu Lys Gly Lys Ser Glu Lys Lys Asn
625 630 635 640

Glu Lys Ser Met Pro Ser Gly Pro Phe Thr Pro Tyr Thr Ser Leu Lys
645 650 655

Lys Glu Gly Phe Glu Cys Ser Lys Tyr Thr Val Glu Arg Val Asn Lys
660 665 670

Ser Cys Gly Val Tyr Tyr Glu Cys Ser Glu Thr Pro Val Leu Phe Thr
675 680 685

Lys Lys Asn Arg Ile Tyr Leu Tyr Ile Ile Leu Ala Val Ser Leu Val
690 695 700

Val Leu Ala Val Leu Ala Tyr Phe Gly Tyr Arg Tyr Tyr Ser Lys Asn
705 710 715 720

His Leu Lys Lys His Asn Ser Gln Ile Tyr Glu Asp Asp Asn Val Asn
725 730 735

Asn Tyr Tyr Asn Glu Asp Phe Asp Asp Glu Gln Asp Arg Asp Glu Tyr
740 745 750

Ala Ser Asn Val Arg Gly Asp Gln Ile Trp Ser Arg His Thr Pro Asp
755 760 765

Arg Ser Glu Val Thr Pro Val Arg Ile Ser Arg Leu Asn His
Page 12

Substitute Sequence Listing

770

775

780

<210> 5
<211> 1968
<212> DNA
<213> Babesia bovis

<220>
<221> CDS
<222> (1)..(1968)

<400> 5
atg atc ggt tac atc aag att ctg gcc tct gtg ccc ctg tta agt tta 48
Met Ile Gly Tyr Ile Lys Ile Leu Ala Ser Val Pro Leu Leu Ser Leu
1 5 10 15
gcc ttt tta gct aca acg ggg ata cat gct ttt gcg gac aaa ggt att 96
Ala Phe Leu Ala Thr Thr Gly Ile His Ala Phe Ala Asp Lys Gly Ile
20 25 30
ggt tca cca aag ggg aaa caa tgc aag aag caa ctt gac ttt tcg att 144
Gly Ser Pro Lys Gly Lys Gln Cys Lys Lys Gln Leu Asp Phe Ser Ile
35 40 45
gtg gta gat gaa tct gct agt ata tcg gat gat caa tgg gag ggt cag 192
Val Val Asp Glu Ser Ala Ser Ile Ser Asp Asp Gln Trp Glu Gly Gln
50 55 60
atg att cca ttt ttg agg aat ttg att cat acc gtt gac ctt gac aac 240
Met Ile Pro Phe Leu Arg Asn Leu Ile His Thr Val Asp Leu Asp Asn
65 70 75 80
act gac ata cgt ctt tcg ctt acc act tac tca act cca act cgc cag 288
Thr Asp Ile Arg Leu Ser Leu Thr Thr Tyr Ser Thr Pro Thr Arg Gln
85 90 95
ata ttt acg ttt ttg gat gct gct gca agc agt acc agg ctc gca ctc 336
Ile Phe Thr Phe Leu Asp Ala Ala Ala Ser Ser Thr Arg Leu Ala Leu
100 105 110
acg aaa ctt gat tgg atg aac ggt acc aaa gct agg tat ggt atg acc 384
Thr Lys Leu Asp Trp Met Asn Gly Thr Lys Ala Arg Tyr Gly Met Thr
115 120 125
tac act ggc agg gct ctg aac tac gtt cgt aag gct ata cta cca tat 432
Tyr Thr Gly Arg Ala Leu Asn Tyr Val Arg Lys Ala Ile Leu Pro Tyr
130 135 140
ggt cgc aag aat gta ccc aag gca ctg tta ctg atc act gat gga gta 480
Gly Arg Lys Asn Val Pro Lys Ala Leu Leu Leu Ile Thr Asp Gly Val
145 150 155 160
tct tcg gat gga agt tac act gca cag gtt gcg gct atg ctt cgt gat 528
Ser Ser Asp Gly Ser Tyr Thr Ala Gln Val Ala Ala Met Leu Arg Asp
165 170 175
gaa ggt gta aat gta atg gtt att ggt gtc ggt gat gta aat gtt gct 576
Glu Gly Val Asn Val Met Val Ile Gly Val Gly Asp Val Asn Val Ala
180 185 190
gaa tgc cgt ggc ata gta gga tgt gat gga ata atg gat tgt cct atg 624

Substitute Sequence Listing															
Glu	Cys	Arg	Gly	Ile	Val	Gly	Cys	Asp	Gly	Ile	Met	Asp	Cys	Pro	Met
		195					200					205			
ttc	aag	cag	acc	aac	tgg	aag	gat	atc	atg	ggc	ctc	ttt	aac	agt	tta
Phe	Lys	Gln	Thr	Asn	Trp	Lys	Asp	Ile	Met	Gly	Leu	Phe	Asn	Ser	Leu
	210					215					220				
atg	aag	gag	gta	tgt	gat	att	tta	cct	cag	gac	gct	gtt	tgt	gag	cct
Met	Lys	Glu	Val	Cys	Asp	Ile	Leu	Pro	Gln	Asp	Ala	Val	Cys	Glu	Pro
	225				230					235					240
gta	tgg	gca	gaa	tgg	tca	tct	tgt	aac	ggg	gaa	tgt	ggc	gtt	cct	ggc
Val	Trp	Ala	Glu	Trp	Ser	Ser	Cys	Asn	Gly	Glu	Cys	Gly	Val	Pro	Gly
				245					250					255	
aaa	cga	act	cgt	gct	ctt	ttg	gac	ctc	cga	atg	att	gaa	aag	ccc	gta
Lys	Arg	Thr	Arg	Ala	Leu	Leu	Asp	Leu	Arg	Met	Ile	Glu	Lys	Pro	Val
			260					265					270		
aat	ggc	tcg	aat	gga	caa	ccg	ggc	aaa	tca	tgt	gag	gat	cag	aag	atg
Asn	Gly	Ser	Asn	Gly	Gln	Pro	Gly	Lys	Ser	Cys	Glu	Asp	Gln	Lys	Met
		275					280					285			
aac	ttc	tta	ccc	caa	tca	gag	aca	tgc	acc	ata	gaa	tgc	aat	cat	gag
Asn	Phe	Leu	Pro	Gln	Ser	Glu	Thr	Cys	Thr	Ile	Glu	Cys	Asn	His	Glu
	290					295					300				
cct	gtg	cca	agc	tcg	ccg	gaa	cct	gta	tca	gat	gat	atg	gat	cac	cca
Pro	Val	Pro	Ser	Ser	Pro	Glu	Pro	Val	Ser	Asp	Asp	Met	Asp	His	Pro
					310					315					320
gaa	cca	act	cct	gtt	aca	ccg	gaa	ggc	gac	atg	gat	aaa	tct	cat	tcc
Glu	Pro	Thr	Pro	Val	Thr	Pro	Glu	Gly	Asp	Met	Asp	Lys	Ser	His	Ser
				325					330					335	
cat	tcg	agc	att	cca	tcc	acc	cct	gat	atg	cca	tca	agt	cac	agt	gat
His	Ser	Ser	Ile	Pro	Ser	Thr	Pro	Asp	Met	Pro	Ser	Ser	His	Ser	Asp
			340					345					350		
atg	tca	tca	agc	cct	act	gat	atg	tca	tca	agc	cct	act	gac	atg	tca
Met	Ser	Ser	Ser	Pro	Thr	Asp	Met	Ser	Ser	Ser	Pro	Thr	Asp	Met	Ser
		355				360						365			
tca	agc	cct	act	gac	atg	tca	tca	agt	cac	agt	gac	atg	cca	tca	act
Ser	Ser	Pro	Thr	Asp	Met	Ser	Ser	Ser	His	Ser	Asp	Met	Pro	Ser	Thr
	370					375					380				
cct	act	ggc	atg	tca	tca	agt	cac	agt	gat	atg	cca	tca	agt	cac	agt
Pro	Thr	Gly	Met	Ser	Ser	Ser	His	Ser	Asp	Met	Pro	Ser	Ser	His	Ser
					390				395						400
gat	atg	cca	tca	agc	cac	agt	gat	atg	tca	tca	agc	cct	act	gac	atg
Asp	Met	Pro	Ser	Ser	His	Ser	Asp	Met	Ser	Ser	Ser	Pro	Thr	Asp	Met
				405					410					415	
tca	tca	agt	cac	gct	gat	act	cgt	gta	gga	aat	acc	gat	gaa	gaa	cat
Ser	Ser	Ser	His	Ala	Asp	Thr	Arg	Val	Gly	Asn	Thr	Asp	Glu	Glu	His
			420					425					430		
aac	cac	agg	aaa	gat	atg	gat	gtc	aag	ttc	ccc	gaa	aat	atg	gat	gat
Asn	His	Arg	Lys	Asp	Met	Asp	Val	Lys	Phe	Pro	Glu	Asn	Met	Asp	Asp
		435					440					445			

Substitute Sequence Listing

atc cca gtc gag gat aat cct ata ccc aca gat cct aga cat ggc gtc Ile Pro Val Glu Asp Asn Pro Ile Pro Thr Asp Pro Arg His Gly Val 450 455 460	1392
gaa cca tcg cct tct gat gtg atc cct gag gat gac caa ctt cgt agg Glu Pro Ser Pro Ser Asp Val Ile Pro Glu Asp Asp Gln Leu Arg Arg 465 470 475 480	1440
acg ctt gaa atg cag cgc gaa gag gac cta aag aag gaa ttg atg ctc Thr Leu Glu Met Gln Arg Glu Glu Asp Leu Lys Lys Glu Leu Met Leu 485 490 495	1488
caa cat gaa ctg aag ctt cag gaa gaa aag gaa agg gca gct att tta Gln His Glu Leu Lys Leu Gln Glu Glu Lys Glu Arg Ala Ala Ile Leu 500 505 510	1536
gag aat aac act cct tat gga tcc gcc act tcc gtg tcg caa gac ggt Glu Asn Asn Thr Pro Tyr Gly Ser Ala Thr Ser Val Ser Gln Asp Gly 515 520 525	1584
gaa tct cca act ggc gta ccc caa agt agc gag acc gat gca ata cgt Glu Ser Pro Thr Gly Val Pro Gln Ser Ser Glu Thr Asp Ala Ile Arg 530 535 540	1632
cac gag gtg tat gac gat cac ccc gag gaa tct gaa aac acc ggg att His Glu Val Tyr Asp Asp His Pro Glu Glu Ser Glu Asn Thr Gly Ile 545 550 555 560	1680
aat gct gat gtg acc gaa tct gag gac tat gag ggt gaa aaa caa aag Asn Ala Asp Val Thr Glu Ser Glu Asp Tyr Glu Gly Glu Lys Gln Lys 565 570 575	1728
gac gaa tca aat gaa cgt tcg acc agc aac act act aag att gcc ggc Asp Glu Ser Asn Glu Arg Ser Thr Ser Asn Thr Thr Lys Ile Ala Gly 580 585 590	1776
ggg gct cta cta ggt ctt ctt ctc ctt ggt gcc ggt ggt gga tac gct Gly Ala Leu Leu Gly Leu Leu Leu Leu Gly Ala Gly Gly Tyr Ala 595 600 605	1824
atg tac aaa aag aac aag aca cct act gtt gag aca ggt tca ggt gat Met Tyr Lys Lys Asn Lys Thr Pro Thr Val Glu Thr Gly Ser Gly Asp 610 615 620	1872
tac act ggg gcc gac gag agt tca gaa ccc atg aag gag ggt gac aca Tyr Thr Gly Ala Asp Glu Ser Ser Glu Pro Met Lys Glu Gly Asp Thr 625 630 635 640	1920
tac acc gtc act gag ttt gac aac aac att tgg ggc gag gca gcg taa Tyr Thr Val Thr Glu Phe Asp Asn Asn Ile Trp Gly Glu Ala Ala 645 650 655	1968

<210> 6
 <211> 655
 <212> PRT
 <213> Babesia bovis

<400> 6

Met Ile Gly Tyr Ile Lys Ile Leu Ala Ser Val Pro Leu Leu Ser Leu
 1 5 10 15

Substitute Sequence Listing

Ala Phe Leu Ala Thr Thr Gly Ile His Ala Phe Ala Asp Lys Gly Ile
20 25 30

Gly Ser Pro Lys Gly Lys Gln Cys Lys Lys Gln Leu Asp Phe Ser Ile
35 40 45

Val Val Asp Glu Ser Ala Ser Ile Ser Asp Asp Gln Trp Glu Gly Gln
50 55 60

Met Ile Pro Phe Leu Arg Asn Leu Ile His Thr Val Asp Leu Asp Asn
65 70 75 80

Thr Asp Ile Arg Leu Ser Leu Thr Thr Tyr Ser Thr Pro Thr Arg Gln
85 90 95

Ile Phe Thr Phe Leu Asp Ala Ala Ala Ser Ser Thr Arg Leu Ala Leu
100 105 110

Thr Lys Leu Asp Trp Met Asn Gly Thr Lys Ala Arg Tyr Gly Met Thr
115 120 125

Tyr Thr Gly Arg Ala Leu Asn Tyr Val Arg Lys Ala Ile Leu Pro Tyr
130 135 140

Gly Arg Lys Asn Val Pro Lys Ala Leu Leu Leu Ile Thr Asp Gly Val
145 150 155 160

Ser Ser Asp Gly Ser Tyr Thr Ala Gln Val Ala Ala Met Leu Arg Asp
165 170 175

Glu Gly Val Asn Val Met Val Ile Gly Val Gly Asp Val Asn Val Ala
180 185 190

Glu Cys Arg Gly Ile Val Gly Cys Asp Gly Ile Met Asp Cys Pro Met
195 200 205

Phe Lys Gln Thr Asn Trp Lys Asp Ile Met Gly Leu Phe Asn Ser Leu
210 215 220

Met Lys Glu Val Cys Asp Ile Leu Pro Gln Asp Ala Val Cys Glu Pro
225 230 235 240

Val Trp Ala Glu Trp Ser Ser Cys Asn Gly Glu Cys Gly Val Pro Gly
245 250 255

Lys Arg Thr Arg Ala Leu Leu Asp Leu Arg Met Ile Glu Lys Pro Val
260 265 270

Substitute Sequence Listing

Asn Gly Ser Asn Gly Gln Pro Gly Lys Ser Cys Glu Asp Gln Lys Met
 275 280 285
 Asn Phe Leu Pro Gln Ser Glu Thr Cys Thr Ile Glu Cys Asn His Glu
 290 295 300
 Pro Val Pro Ser Ser Pro Glu Pro Val Ser Asp Asp Met Asp His Pro
 305 310 315 320
 Glu Pro Thr Pro Val Thr Pro Glu Gly Asp Met Asp Lys Ser His Ser
 325 330 335
 His Ser Ser Ile Pro Ser Thr Pro Asp Met Pro Ser Ser His Ser Asp
 340 345 350
 Met Ser Ser Ser Pro Thr Asp Met Ser Ser Ser Pro Thr Asp Met Ser
 355 360 365
 Ser Ser Pro Thr Asp Met Ser Ser Ser His Ser Asp Met Pro Ser Thr
 370 375 380
 Pro Thr Gly Met Ser Ser Ser His Ser Asp Met Pro Ser Ser His Ser
 385 390 395 400
 Asp Met Pro Ser Ser His Ser Asp Met Ser Ser Ser Pro Thr Asp Met
 405 410 415
 Ser Ser Ser His Ala Asp Thr Arg Val Gly Asn Thr Asp Glu Glu His
 420 425 430
 Asn His Arg Lys Asp Met Asp Val Lys Phe Pro Glu Asn Met Asp Asp
 435 440 445
 Ile Pro Val Glu Asp Asn Pro Ile Pro Thr Asp Pro Arg His Gly Val
 450 455 460
 Glu Pro Ser Pro Ser Asp Val Ile Pro Glu Asp Asp Gln Leu Arg Arg
 465 470 475 480
 Thr Leu Glu Met Gln Arg Glu Glu Asp Leu Lys Lys Glu Leu Met Leu
 485 490 495
 Gln His Glu Leu Lys Leu Gln Glu Glu Lys Glu Arg Ala Ala Ile Leu
 500 505 510
 Glu Asn Asn Thr Pro Tyr Gly Ser Ala Thr Ser Val Ser Gln Asp Gly
 Page 17

515

```
<210> 7
<211> 1047
<212> DNA
<213> Theileria annulata
```

<220>
<221> CDS
<222> (1)..(1047)

[illegible]

Substitute Sequence Listing															
Phe 65	Ser	Thr	Ser	Ile	Arg 70	Trp	Leu	Ile	Ser	Phe 75	Leu	Asp	Pro	Ala	Ser 80
aag Lys	gat Asp	gag Glu	caa Gln	ttg Leu 85	gcc Ala	ctt Leu	gct Ala	gtt Val	ctg Leu 90	gac Asp	aag Lys	ctg Leu	aag Lys	aac Asn 95	agt Ser
aag Lys	cct Pro	gtg Val	ttt Phe 100	ggg Gly	tac Tyr	aca Thr	ttc Phe	act Thr 105	gga Gly	cag Gln	gca Ala	ctt Leu	aac Asn 110	ttt Phe	att Ile
tct Ser	gag Glu	gct Ala 115	gtt Val	tat Tyr	atg Met	ttt Phe	ggt Gly 120	gct Ala	agg Arg	cgt Arg	aac Asn	tct Ser 125	cca Pro	aag Lys	ggc Gly
atc Ile 130	att Ile	atc Ile	atc Ile	acc Thr	gac Asp	gga Gly 135	tcc Ser	tct Ser	act Thr	cag Gln	aca Thr 140	aac Asn	gtt Val	act Thr	tct Ser
cag Gln 145	gcg Ala	tcg Ser	gct Ala	cta Leu	cta Leu 150	agg Arg	gat Asp	gct Ala	ggt Gly	gta Val 155	aca Thr	att Ile	cta Leu	gtt Val	gtt Val 160
gga Gly	gtt Val	ggg Gly	aag Lys	gct Ala 165	aaa Lys	gaa Glu	agc Ser	gag Glu	tgt Cys 170	aga Arg	ggt Gly	ata Ile	gtt Val	ggt Gly 175	tgt Cys
tct Ser	acc Thr	aaa Lys	gga Gly 180	gag Glu	tgc Cys	ccc Pro	ctt Leu	ttc Phe 185	ttt Phe	atg Met	acc Thr	aac Asn	tgg Trp 190	gat Asp	gaa Glu
att Ile	atc Ile	agg Arg 195	aag Lys	gtt Val	ggg Gly	gag Glu	ttg Leu 200	atg Met	gct Ala	gag Glu	gtt Val	tgt Cys 205	gag Glu	acc Thr	att Ile
cct Pro	aag Lys 210	gac Asp	gcc Ala	gta Val	tgt Cys	aag Lys 215	ccg Pro	atc Ile	tgg Trp	tct Ser	gat Asp 220	tgg Trp	tct Ser	aag Lys	tgt Cys
gac Asp 225	gcc Ala	aag Lys	tgc Cys	ggc Gly	att Ile 230	ggg Gly	acg Thr	agg Arg	tac Tyr	caa Gln 235	aag Lys	ttg Leu	atg Met	gga Gly	gtt Val 240
act Thr	aca Thr	att Ile	tct Ser	gag Glu 245	cca Pro	act Thr	gtc Val	gga Gly	acg Thr 250	aac Asn	ggc Gly	aag Lys	tcc Ser	ggg Gly 255	agg Arg
aca Thr	tgt Cys	gag Glu	atg Met 260	att Ile	tat Tyr	gag Glu	aac Asn	gtc Val 265	gag Glu	gtt Val	cca Pro	aag Lys	gag Glu 270	gag Glu	tgc Cys
tcc Ser	gtt Val	gag Glu 275	tct Ser	aag Lys	att Ile	gct Ala	gga Gly 280	gga Gly	gtg Val	gct Ala	cta Leu 285	gca Ala	ctg Leu	tta Leu	atg Met
ctt Leu	gca Ala 290	ggc Gly	gga Gly	ggt Gly	ggt Gly	tac Tyr 295	aca Thr	tac Tyr	tac Tyr	aaa Lys	aag Lys 300	tac Tyr	ggt Gly	tta Leu	tct Ser
aga Arg 305	gtg Val	agt Ser	gaa Glu	act Thr	acg Thr 310	aat Asn	ttg Leu	gat Asp	gag Glu 315	gat Asp	ttt Phe	gca Ala	gat Asp	tct Ser	agt Ser 320

Substitute Sequence Listing

ggg aac cgt ggt gta agg gag agt gtg ggt gaa gct tac aca gta act 1008
Gly Asn Arg Gly Val Arg Glu Ser Val Gly Glu Ala Tyr Thr Val Thr 335
325 330

gat tta gat gat gga ctc tgg agc caa tcc aat caa taa 1047
Asp Leu Asp Asp Gly Leu Trp Ser Gln Ser Asn Gln 345
340

<210> 8
<211> 348
<212> PRT
<213> Theileria annulata

<400> 8

Asp Lys Gly Leu Tyr Pro Asp Gly Ile Lys Lys Pro Ser Ser Tyr Cys
1 5 10 15

His Arg Glu Leu Asp Leu Thr Ile Leu Val Asp Glu Ser Ser Ser Ile
20 25 30

Tyr Ile Glu Glu Trp Asn Lys Leu Ile Pro Phe Leu Lys Ser Leu Val
35 40 45

Arg Ser Ile Asn Ile Ser Pro Asn Tyr Val His Leu Ser Met Val Thr
50 55 60

Phe Ser Thr Ser Ile Arg Trp Leu Ile Ser Phe Leu Asp Pro Ala Ser
65 70 75 80

Lys Asp Glu Gln Leu Ala Leu Ala Val Leu Asp Lys Leu Lys Asn Ser
85 90 95

Lys Pro Val Phe Gly Tyr Thr Phe Thr Gly Gln Ala Leu Asn Phe Ile
100 105 110

Ser Glu Ala Val Tyr Met Phe Gly Ala Arg Arg Asn Ser Pro Lys Gly
115 120 125

Ile Ile Ile Ile Thr Asp Gly Ser Ser Thr Gln Thr Asn Val Thr Ser
130 135 140

Gln Ala Ser Ala Leu Leu Arg Asp Ala Gly Val Thr Ile Leu Val Val
145 150 155 160

Gly Val Gly Lys Ala Lys Glu Ser Glu Cys Arg Gly Ile Val Gly Cys
165 170 175

Ser Thr Lys Gly Glu Cys Pro Leu Phe Phe Met Thr Asn Trp Asp Glu
180 185 190

Substitute Sequence Listing

Ile Ile Arg Lys Val Gly Glu Leu Met Ala Glu Val Cys Glu Thr Ile
195 200 205

Pro Lys Asp Ala Val Cys Lys Pro Ile Trp Ser Asp Trp Ser Lys Cys
210 215 220

Asp Ala Lys Cys Gly Ile Gly Thr Arg Tyr Gln Lys Leu Met Gly Val
225 230 235 240

Thr Thr Ile Ser Glu Pro Thr Val Gly Thr Asn Gly Lys Ser Gly Arg
245 250 255

Thr Cys Glu Met Ile Tyr Glu Asn Val Glu Val Pro Lys Glu Glu Cys
260 265 270

Ser Val Glu Ser Lys Ile Ala Gly Gly Val Ala Leu Ala Leu Leu Met
275 280 285

Leu Ala Gly Gly Gly Gly Tyr Thr Tyr Tyr Lys Lys Tyr Gly Leu Ser
290 295 300

Arg Val Ser Glu Thr Thr Asn Leu Asp Glu Asp Phe Ala Asp Ser Ser
305 310 315 320

Gly Asn Arg Gly Val Arg Glu Ser Val Gly Glu Ala Tyr Thr Val Thr
325 330 335

Asp Leu Asp Asp Gly Leu Trp Ser Gln Ser Asn Gln
340 345

<210> 9
<211> 2259
<212> DNA
<213> Babesia bovis

<220>
<221> CDS
<222> (552)..(2189)

<220>
<221> misc_feature
<222> (1465)..(1465)
<223> The 'r' at location 1465 stands for g or a

<400> 9
ataagatgta gcactgatgt gtgtactcgg actctgacac tggagtatag gctaccagaa 60
ctgggcgcaa ctcctaata gtagtgccgt cccaggaggc cacagaacaa tggagtacaa 120
cgctcaaaac cgagtgtaat gttagctaca atatgtacat attgtcatgg agttcgtaat 180

Substitute Sequence Listing

cctaacaaag gccattgtat cgtcaatgtg gtctaccagt ggacgtcgct tgtggaggcc	240
agggtacatc aaatccctga gaacacctat cgtccggtgt tacggtggta atgggttact	300
ataaaagcaa atttaattgt agatattgta aaaaaactgt aaaattgggtt agtgcttgca	360
ccgtcctgggt cccgcgatttt ggataccgct gtgctacgct ttgcacggaa tcacgacgct	420
gtgcataacg ctgtgcttat gacttcgtac acatcaaacg actttaactg ccgttggttt	480
atatacgttg gcgttaggtt gttttgggtg ttattgtact gtggaatcat acacattcta	540
cacgtgtcat g atg gtg aag ttc cac aca tta tcg gtt gca gcc atc ctg	590
Met Val Lys Phe His Thr Leu Ser Val Ala Ala Ile Leu	
1 5 10	
gcg att gct tca tcc aat act att ttt gct aca ttt aga tca aat gga	638
Ala Ile Ala Ser Ser Asn Thr Ile Phe Ala Thr Phe Arg Ser Asn Gly	
15 20 25	
aaa acc ttc gga gat gaa tct gtt agc ctt cta gaa cat gaa agt acc	686
Lys Thr Phe Gly Asp Glu Ser Val Ser Leu Leu Glu His Glu Ser Thr	
30 35 40 45	
agt ttg tct cgt ggt cct aga cca acc gaa gat caa atc agt cag tta	734
Ser Leu Ser Arg Gly Pro Arg Pro Thr Glu Asp Gln Ile Ser Gln Leu	
50 55 60	
cca aaa aat gtt ttc ttt cta ttg gat aac agc att gat atg tct att	782
Pro Lys Asn Val Phe Phe Leu Leu Asp Asn Ser Ile Asp Met Ser Ile	
65 70 75	
gaa act gga gaa gag aat cgt cat ttc ctc tcc gag ttt ttt aaa ttg	830
Glu Thr Gly Glu Glu Asn Arg His Phe Leu Ser Glu Phe Phe Lys Leu	
80 85 90	
tta aaa aaa tat gaa gga ata aat gtt tca cta ata agg tac aat agt	878
Leu Lys Lys Tyr Glu Gly Ile Asn Val Ser Leu Ile Arg Tyr Asn Ser	
95 100 105	
gaa gaa ccg tta ggt tcg acg aaa gca tta acc aac ggg gag ttg aaa	926
Glu Glu Pro Leu Gly Ser Thr Lys Ala Leu Thr Asn Gly Glu Leu Lys	
110 115 120 125	
aaa cta tcc gat aat att cct act aaa atg cct ttt gac att ggc gtt	974
Lys Leu Ser Asp Asn Ile Pro Thr Lys Met Pro Phe Asp Ile Gly Val	
130 135 140	
gtt cct act ggt ata gga gct gcc ctc aaa cag ata aaa aca ttg tac	1022
Val Pro Thr Gly Ile Gly Ala Ala Leu Lys Gln Ile Lys Thr Leu Tyr	
145 150 155	
cct gat cac gaa aag ttc ctt gtt ggg aac acc att act gag ttg gat	1070
Pro Asp His Glu Lys Phe Leu Val Gly Asn Thr Ile Thr Glu Leu Asp	
160 165 170	
tat tct aaa gca ttg ggt aag gat att gtt gta atc gtg ttt act act	1118
Tyr Ser Lys Ala Leu Gly Lys Asp Ile Val Val Ile Val Phe Thr Thr	
175 180 185	
ggc cac gtc att gat cca tat tta gca tat gat gag gca ttt gat gcc	1166
Gly His Val Ile Asp Pro Tyr Leu Ala Tyr Asp Glu Ala Phe Asp Ala	
190 195 200 205	

Substitute Sequence Listing

cgc	cgt	aat	ggt	gta	aga	ttt	tac	gtt	att	aat	agg	gga	gga	aag	gca	1214
Arg	Arg	Asn	Gly	Val	Arg	Phe	Tyr	Val	Ile	Asn	Arg	Gly	Gly	Lys	Ala	
				210					215					220		
aaa	aac	tat	tgg	act	cag	cta	ttg	gga	tgc	cac	tac	aat	act	tgt	ttg	1262
Lys	Asn	Tyr	Trp	Thr	Gln	Leu	Leu	Gly	Cys	His	Tyr	Asn	Thr	Cys	Leu	
			225					230					235			
agt	tat	att	cgg	gcc	aaa	ata	aca	agg	cct	tca	cta	tat	ctc	gat	gtt	1310
Ser	Tyr	Ile	Arg	Ala	Lys	Ile	Thr	Arg	Pro	Ser	Leu	Tyr	Leu	Asp	Val	
		240					245					250				
ttg	gtg	aac	agg	att	gtg	tct	aaa	cgc	gcg	aaa	gat	gcc	gtt	tgt	ttg	1358
Leu	Val	Asn	Arg	Ile	Val	Ser	Lys	Arg	Ala	Lys	Asp	Ala	Val	Cys	Leu	
	255					260					265					
gaa	gtg	tgg	acg	gat	tat	aaa	cct	aac	act	gaa	aaa	tcg	gat	gtg	agg	1406
Glu	Val	Trp	Thr	Asp	Tyr	Lys	Pro	Asn	Thr	Glu	Lys	Ser	Asp	Val	Arg	
					275					280					285	
att	atg	act	tct	acg	ttg	aaa	tta	tac	aaa	acc	ctt	ctt	act	gga	agc	1454
Ile	Met	Thr	Ser	Thr	Leu	Lys	Leu	Tyr	Lys	Thr	Leu	Leu	Thr	Gly	Ser	
				290					295					300		
ttt	gcg	gag	ara	aac	atc	aaa	ggt	ctc	aca	tgt	gat	gag	cag	cta	aag	1502
Phe	Ala	Glu	Xaa	Asn	Ile	Lys	Gly	Leu	Thr	Cys	Asp	Glu	Gln	Leu	Lys	
			305					310					315			
gat	atg	cag	aaa	aga	caa	ata	ttt	tgc	tac	tca	aat	aag	tgt	gct	ccc	1550
Asp	Met	Gln	Lys	Arg	Gln	Ile	Phe	Cys	Tyr	Ser	Asn	Lys	Cys	Ala	Pro	
			320				325					330				
acg	atc	tat	tca	aga	tct	tat	gtt	gac	tta	gct	att	caa	cgt	ctt	aat	1598
Thr	Ile	Tyr	Ser	Arg	Ser	Tyr	Val	Asp	Leu	Ala	Ile	Gln	Arg	Leu	Asn	
	335					340					345					
gca	aaa	gat	ttt	aaa	gag	gta	cta	gat	gag	tca	tct	tac	aga	tca	cgc	1646
Ala	Lys	Asp	Phe	Lys	Glu	Val	Leu	Asp	Glu	Ser	Ser	Tyr	Arg	Ser	Arg	
					355				360						365	
agt	ttg	caa	tca	gtg	gag	aaa	cat	aat	gag	caa	caa	aca	ggt	tct	caa	1694
Ser	Leu	Gln	Ser	Val	Glu	Lys	His	Asn	Glu	Gln	Gln	Thr	Gly	Ser	Gln	
				370					375					380		
gaa	acg	ctt	tct	gga	agc	gcc	cgt	gta	gaa	aca	agc	tta	gaa	agc	tca	1742
Glu	Thr	Leu	Ser	Gly	Ser	Ala	Arg	Val	Glu	Thr	Ser	Leu	Glu	Ser	Ser	
			385					390					395			
gta	cct	tca	tcc	tat	gtg	gca	gaa	ttg	gga	gaa	agt	gat	aca	gaa	aca	1790
Val	Pro	Ser	Ser	Tyr	Val	Ala	Glu	Leu	Gly	Glu	Ser	Asp	Thr	Glu	Thr	
			400				405					410				
tac	aaa	cag	ttg	gag	tac	ata	gat	aaa	aat	ggc	gtc	act	gtc	ttc	aac	1838
Tyr	Lys	Gln	Leu	Glu	Tyr	Ile	Asp	Lys	Asn	Gly	Val	Thr	Val	Phe	Asn	
	415					420					425					
gat	gag	ccc	act	gtt	gtt	gtc	gat	act	ccc	gag	tac	gta	caa	aag	gtg	1886
Asp	Glu	Pro	Thr	Val	Val	Val	Asp	Thr	Pro	Glu	Tyr	Val	Gln	Lys	Val	
					435					440					445	
cat	gaa	aga	gaa	atg	cag	ttt	gat	gaa	gaa	tcc	acc	cat	ctt	ccc	aac	1934
His	Glu	Arg	Glu	Met	Gln	Phe	Asp	Glu	Glu	Ser	Thr	His	Leu	Pro	Asn	

Substitute Sequence Listing

450	455	460	
tct ggt aac cac cat cca cct cat cac cga aag ggg gcc aac gga tcc			1982
Ser Gly Asn His His Pro Pro His His Arg Lys Gly Ala Asn Gly Ser			
	465	475	
ggt aaa aag acc acg atc gtc gtt ggt att ata tgc ctt gta gta ata			2030
Gly Lys Lys Thr Thr Ile Val Val Gly Ile Ile Cys Leu Val Val Ile			
	480	490	
tgc gcc gtc ata gcc ggc gcc tac cta tcc ctt tca cag caa gag tct			2078
Cys Ala Val Ile Ala Gly Ala Tyr Leu Ser Leu Ser Gln Gln Glu Ser			
	495	505	
gtg gaa ctc acc tct gaa gag ggt gac ttc ttg aac gac act acg ggt			2126
Val Glu Leu Thr Ser Glu Glu Gly Asp Phe Leu Asn Asp Thr Thr Gly			
	510	520	525
ggt caa cct gag gta ctc gaa aca caa cag gtt gtg gat gca gag aac			2174
Gly Gln Pro Glu Val Leu Glu Thr Gln Val Val Asp Ala Glu Asn			
	530	535	540
aaa aca tgg ttg taa gacacgaaac gggttgtcac agccaacata taaaaatgca			2229
Lys Thr Trp Leu			
	545		
gtttaaatta agtcactagt taaaaaaaaa			2259

<210> 10
 <211> 545
 <212> PRT
 <213> Babesia bovis

<220>
 <221> misc_feature
 <222> (305)..(305)
 <223> The 'Xaa' at location 305 stands for Arg, or Lys.

<400> 10

Met Val Lys Phe His Thr Leu Ser Val Ala Ala Ile Leu Ala Ile Ala
 1 5 10 15

Ser Ser Asn Thr Ile Phe Ala Thr Phe Arg Ser Asn Gly Lys Thr Phe
 20 25 30

Gly Asp Glu Ser Val Ser Leu Leu Glu His Glu Ser Thr Ser Leu Ser
 35 40 45

Arg Gly Pro Arg Pro Thr Glu Asp Gln Ile Ser Gln Leu Pro Lys Asn
 50 55 60

Val Phe Phe Leu Leu Asp Asn Ser Ile Asp Met Ser Ile Glu Thr Gly
 65 70 75 80

Glu Glu Asn Arg His Phe Leu Ser Glu Phe Phe Lys Leu Leu Lys Lys
 85 90 95

Substitute Sequence Listing

Tyr Glu Gly Ile Asn Val Ser Leu Ile Arg Tyr Asn Ser Glu Glu Pro
 100 105 110
 Leu Gly Ser Thr Lys Ala Leu Thr Asn Gly Glu Leu Lys Lys Leu Ser
 115 120 125
 Asp Asn Ile Pro Thr Lys Met Pro Phe Asp Ile Gly Val Val Pro Thr
 130 135 140
 Gly Ile Gly Ala Ala Leu Lys Gln Ile Lys Thr Leu Tyr Pro Asp His
 145 150 155 160
 Glu Lys Phe Leu Val Gly Asn Thr Ile Thr Glu Leu Asp Tyr Ser Lys
 165 170 175
 Ala Leu Gly Lys Asp Ile Val Val Ile Val Phe Thr Thr Gly His Val
 180 185 190
 Ile Asp Pro Tyr Leu Ala Tyr Asp Glu Ala Phe Asp Ala Arg Arg Asn
 195 200 205
 Gly Val Arg Phe Tyr Val Ile Asn Arg Gly Gly Lys Ala Lys Asn Tyr
 210 215 220
 Trp Thr Gln Leu Leu Gly Cys His Tyr Asn Thr Cys Leu Ser Tyr Ile
 225 230 235 240
 Arg Ala Lys Ile Thr Arg Pro Ser Leu Tyr Leu Asp Val Leu Val Asn
 245 250 255
 Arg Ile Val Ser Lys Arg Ala Lys Asp Ala Val Cys Leu Glu Val Trp
 260 265 270
 Thr Asp Tyr Lys Pro Asn Thr Glu Lys Ser Asp Val Arg Ile Met Thr
 275 280 285
 Ser Thr Leu Lys Leu Tyr Lys Thr Leu Leu Thr Gly Ser Phe Ala Glu
 290 295 300
 Xaa Asn Ile Lys Gly Leu Thr Cys Asp Glu Gln Leu Lys Asp Met Gln
 305 310 315 320
 Lys Arg Gln Ile Phe Cys Tyr Ser Asn Lys Cys Ala Pro Thr Ile Tyr
 325 330 335
 Ser Arg Ser Tyr Val Asp Leu Ala Ile Gln Arg Leu Asn Ala Lys Asp

Substitute Sequence Listing

340
 Phe Lys Glu Val Leu Asp Glu Ser Ser Tyr Arg Ser Arg Ser Leu Gln
 355 360 365
 Ser Val Glu Lys His Asn Glu Gln Gln Thr Gly Ser Gln Glu Thr Leu
 370 375 380
 Ser Gly Ser Ala Arg Val Glu Thr Ser Leu Glu Ser Ser Val Pro Ser
 385 390 395 400
 Ser Tyr Val Ala Glu Leu Gly Glu Ser Asp Thr Glu Thr Tyr Lys Gln
 405 410 415
 Leu Glu Tyr Ile Asp Lys Asn Gly Val Thr Val Phe Asn Asp Glu Pro
 420 425 430
 Thr Val Val Val Asp Thr Pro Glu Tyr Val Gln Lys Val His Glu Arg
 435 440 445
 Glu Met Gln Phe Asp Glu Glu Ser Thr His Leu Pro Asn Ser Gly Asn
 450 455 460
 His His Pro Pro His His Arg Lys Gly Ala Asn Gly Ser Gly Lys Lys
 465 470 475 480
 Thr Thr Ile Val Val Gly Ile Ile Cys Leu Val Val Ile Cys Ala Val
 485 490 495
 Ile Ala Gly Ala Tyr Leu Ser Leu Ser Gln Gln Glu Ser Val Glu Leu
 500 505 510
 Thr Ser Glu Glu Gly Asp Phe Leu Asn Asp Thr Thr Gly Gly Gln Pro
 515 520 525
 Glu Val Leu Glu Thr Gln Gln Val Val Asp Ala Glu Asn Lys Thr Trp
 530 535 540

Leu
545

<210> 11
 <211> 22
 <212> DNA
 <213> Artificial

<220>
 <223> primer 1

Substitute Sequence Listing

<400> 11		
ccacggctct ggaatctatg tc		22
<210> 12		
<211> 24		
<212> DNA		
<213> Artificial		
<220>		
<223> primer 2		
<400> 12		
caaaaggata cctatatattg gtac		24
<210> 13		
<211> 27		
<212> DNA		
<213> Artificial		
<220>		
<223> Primer 3		
<400> 13		
tgtggtagat gaatctgcta gtatatc		27
<210> 14		
<211> 27		
<212> DNA		
<213> Artificial		
<220>		
<223> Primer 4		
<400> 14		
ctatgccacg gcattcagca acattta		27
<210> 15		
<211> 27		
<212> DNA		
<213> Artificial		
<220>		
<223> Primer 5		
<400> 15		
cccggatcca tgcagttaca taacaaa		27
<210> 16		
<211> 27		
<212> DNA		
<213> Artificial		
<220>		
<223> Primer 6		
<400> 16		
gggaagcttc tgagcaaagg aaatagg		27

Substitute Sequence Listing

<210> 17
 <211> 27
 <212> DNA
 <213> Artificial

<220>
 <223> Primer 7

<400> 17
 cccgaattcg tggtagatga atctgct 27

<210> 18
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <223> Primer 8

<400> 18
 cccgtcgact gcctcgcccc aaatgttgt 29

<210> 19
 <211> 30
 <212> DNA
 <213> Artificial

<220>
 <223> Primer 9

<400> 19
 cccgaattcc atgatggtga agttccacac 30

<210> 20
 <211> 29
 <212> DNA
 <213> Artificial

<220>
 <223> Primer 10

<400> 20
 cccgtcgacg ttggccccct ttcggtgat 29